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Consensus includes gb.Av. 2002 in EXTS, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC ESTS SIGNER To Z132_HUMAN ZINC ESTS SIGNER TO Z132_HUMA	Consensus includes gb.b.Pop. 2017. CONE=IMAGE: 4286422 /UG=Hs. 55098 EST syttytaaagcaaccacttttaaataattacagagtaattattaccctattgaattaaggagataggaaattgaaattcagcagttaattatcagagtaattattaccctattgaattaaggagataggaaattgaaattcagcagtttaattataataattaat	ESTsatagatagatagatagtitggagtittggataaaaatcicgagtitgagatctgagagaccattctnagggagtitgtgagatgaccaagatttgaaccatggtaaacattggagaggacattctaggtggaaggaa

	03)443		FC 1/EFU2/12303
235124 at	235101_at	235061 at	
ab BE502930	gb AV683244	gb AV706522	
Consensus includes gb. 5500, 1	Consensus includes gb:AV683244 /rEA=EST //DB_ANEF=9t.1926302 //JG=Hs.195602 EST saaaaaaaaaaaaaaaaaaaaaaaaaaaattattaaacattaaaaaa	Consensus includes gb:AV / 0522 / FENERAL DEFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILT SQ SEQUENCE CONTAMINE //UG=Hs.291000 ESTs, Moderately sim	gacaggaggatggcagagaaacaactgtcaatccagatttgacctcatttgcattgcaccaaggcctctaggaaaaangaaggaatttlatcccagagagaaacaactgtcaatccagatttgacctcatttgccaccaaggccatcaaggagttcccttattcccagggggtgcccatattcccaatactgtaaagcagcaggaattttatcccagggggtgcccatattcccaatactgtaaagcagcaggaccattattcccagggggtgccatattcccaatactgtaaagcaatccttaactgtaaggcaattttacccagggggtgccatattgaccatatttgtacagaacactattaggcaggtattttagcacctcgccaaggagccatattgaccaggattcaaggcaggtatctctgcaaattgtgcatccgtgaatgtggcaggttgcaggattcaggattcaggaatcaggaattcaggaattcaggaattgcaaggattgcaaggaattgcaggattggaattgtgaattttggaatttggaatttggaatttggaatttggaatttggaatttggaatttggaatttggaatttggaatttggaattttaaggaattaatttaaggaattaatttaaggaattaattaaggaatttaaggaatttaaggaatttaaggaatttaaggaatttaaggaatttaaggaatttaaggaattaattaagaatttaagaattaattaagaattaataa

WO 03/0)39443		PCT/EP02/12303
235278_at	235263_at	235259 at	
gb BF032500	gb BF530545	gb AA398590	
Consensus includes gp. br 032300 // EARLO 7002/11 gr. // CLONE=IMAGE:3856854 /UG=Hs.136585 // CLONE=IMAGE:3856854 /UG=Hs.136585 // CLONE=IMAGE:3856854 /UG=Hs.136585 // CLONE=IMAGE:3856854 /UG=Hs.136585	Consensus includes gb. br. 30043 if Co. 100 Co	Consensus includes gb:AA398590 /FEA=ES1 /DB_XREF-91.2031032 /DB_XREF-91.2031032 /DB_XREF-91.2031032 /DB_XREF-91.2031032 /DB_XREF-91.2031032 /DB_XREF-91.2031032 /DB_XREF-91.2031032 /DB_XREF-91.2031032 /DB_XREF-91.203103 /DB_XREF-91.203103 /DB_XREF-91.203103 /DB_XREF-91.203103 /DB_XREF-91.203103 /DB_XREF-91.203103 /DB_XREF-91.5031103 /DB_XREF-91.	H. sapiensgaccagtactggagtmnnngtmnnngnannncnncgcccgactctgggcccgggtaggaacaaacaatttcggacctctnggggtctatgctaggtatgaggtacttctgggtatcnttgccctccatcaagtagcaaagatggacatgtaaacaaatttcgacactgtgatgactgccacaaaaagcagcantatgaggttgaatgtnacnaggataaccttagcgggtggttgaactgaagtgactgccacaaaaagcagcantatgaggttgaatgtnacnaggataaccttagcggcgggggggggg

gatggcgactaagaggcgaaaactttcggtgtctgaactgctcagcticgca	ab A 341142	235331 x at
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acacacaaaaaaaa	gb BE875232	235291 s at
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EST saaggatccagaatgggacggattcgucctcaggatcagcctcacggattctaggctagcggtcaacaaccgcatccctcgggaacctggaaactctaggtccgaggatctcg tccttccacaccacctctctgtcctaggccttcgtcccggttcagccctcacggattctaggctgtccgtcc		
Consensus includes guine of 1222 in the consensus guine gui		
caaaaataatcaaaa	gb AW192700	235287_at
catgcctaagaacgricargaaaaaaaaaaaaaaaaaaaaaaaaaaa		
anaggaaattctggagaaaacaaatgttatgaagagatgtcccaagcaaactaaattacctgtactttttcccatttcaagggaagaggcaaccacatgaagcaatacttcuaca gtgggattaatatggtcgaaaacaaatgttatgaagagcatgtcccaagcaaactaaattacctgtactttttccaatttacccaagaggaagaggcaaccacttatcatgtccattaagtatatttg		
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Consensus includes gb:AW192700 /FEA=EST /UB_AREF-9:.047 1333 /UE_AREF-9:.047 1333 /UE_AREF-		
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aaatggcttctgatatctggtataaactgctaaataggaraataaggiccuunguaaaceggarnatgtgaaaannanaaannanaaannnnnnnnnaaaaaaaa		
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235372_at	235359 at	235353 at	
gb AW575245	gbJA534416	gb Al887866	
udes gb:AW575245		Consensus includes gb:Al86/866/FEA=EST/DB_ANET_PI-20100000000000000000000000000000000000	atogaccaagaattgattloggttagaccaagggggcccagacctcactgagattgaatcctgcactattgttactcgtcaacagattgcacagttaacggtgtgaaccaagggggccatngtcatctintaaattgtcagttgcattcattgttattctgttaattgtgagcaaaccagatttcagcattgtcaacagtgccatngtctatcintaaattgtcagttgcagttgttctattaggagcaaaccaagtgccattctgcnactgaaccatctgcataaggattattgttgttgttgttaattacactagttagt

WO 03/039443		PCT/EP02/12303
235400 at	235385 at	
gb AL560266	gb Al935334	
(5 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (6 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (7 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (8 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (9 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (1 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (1 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (1 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (2 prime) //UG=Hs.266331 ESTs,	Consensus includes gb:Al93334 / FEX-EX / DE_YEX / PURE / P	/CLONE=IMAGE:3055360 /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma H. sapiensaatagaataaacagttcatccatatctcactnaccaccccaataaatctgattctttattttctcttcctgtcctgcacatatgcataagttactttacaagtngtccaagtttttactattttcttacttgcaccaacagaattctgcttttacaagtngtccaagtttttttttt

0/0/0 5	gb AA977218	on at
Consensus includes gb.AV / 13002 / 15072 / 150	gb AV713062	235421_at
Consensus includes gb:BH-4325/1 /FEA=ES1 //DE //NET-YEST //DE	gb BF432571	<u>.</u>
Consensus includes gb:AL560266 /FEA=EST /DB_XREF=gi:12906564 /DB_XREF=est.AL500200 /CCOXEGUARD (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (6 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma (7 prime) /UG=Hs.266310 ESTs, Weakly similar to A39878 Fc gamma (7 prime) /UG=Hs.266310 ESTs, Weakly similar to A39878 Fc gamma (7 prime) /UG=Hs.266310 ESTs, Weakly similar to A39878 Fc gamma (7 prime) /UG=Hs.266310 ESTs, W	gb AL560266	

Consensus includes your intervent — //UG=Hs.136316 ESTsagfgcttttccccccttaaactcctttaaaattacttttagaacttgctgctcattcttgtgaatgttatg cattgaatgtctgccctgtgagatactcactagagtgaacatgaggaggcttatgtagcaaaatggcac	ab BF114745	235450 at
	gb AW856618	235446 at
Consensus includes gr. All 1907 in the consensus includes grant and careful grant and care	gb A 417897	235444 at
Consensus includes gb:H/8109/FEX=EST/DB_XREF=gi:4261401/DB_XREF=est:tg55b06.x1 /CLONE=IMAGE:2112659	gb H78106	235428_at
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32,322 110				
22 E	235521 at	235502_at	235483_at	
chiai758697	gb)AW137982	gb BF030448	gb AA858058	
	Consensus includes gb.Avv 13 732 / EA-CONE-IMAGE:2714461 /UG=Hs.222446 //CLONE=IMAGE:2714461 /UG=Hs.222446 //CLONE=IMAGE:2714461 /UG=Hs.222446 EST sctgcagaagtgatagtgggcttggggctagggcgccagggaggtctccccccaccca	Consensus includes gb:BF030446 /FEA=E31 /DB_XNEF=gi:BF0706 / CLONE=IMAGE:3828250 /UG=Hs.79204 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE /CLONE=IMAGE:3828250 /UG=Hs.79204 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY CONTAMINATION WARNING ENTRY H.sapiensactttgggagaccagggttgggttgggttggagaccaggaggttgcagaccatctctacaaaaaatagaaaattattgaaaattattggaaaattattgaaaattatt	Consensus includes gb:AA858058 /FEA=E31 /DB_ANE-19:2010000000000000000000000000000000000	atcataaatgtgctaagtggatttactagtaatatgtgagccaaggacgataaagctcctgattctgatgggtarcaggaaaggciiiicaggaaggciiiicaggaaggaaggtaacaactgctgctittgtaaaaaactttattggaatacagttatgccaactgntttatanannnnnnnnnn

WO 03/039443			PCT/EP	02/12303
235706 at	235692 at	235674 at	235647 at	
gb AW663908	gb AW024527	gb AW575183	gb]Al298279	
Consensus includes gb:Avvoo3906 / FEXTEX BY ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTs, Moderately similar to ALUY_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING //UG=Hs.241569 ESTS, MODERATELY SQ SEQUENCE CONTAMINATION W	Consensus includes gb:AW02452/ /FEA=EST /DB_XREF=ni-7456447 /DB_XREF=est.hir3do8.x1 /CLONE=IMAGE:2977935	Consensus includes gb:AVV5751637FEA-E317DE-XNET 9:77 FEA-E317DE-XNET 9:7	Consensus includes gb:Al298Z/9 /FEA=E31 /Db_XNEF=91.330010 /DC=Hs.293411 /UG=Hs.293411 ESTsccaactacttgggaggctgtgggaggatcacttgaacccaggagacagaggttgcggttgagttgagattgagattgtgccactgcactccagcctgggcacagaggtg agattccgtctcaaaaaaaaaa	gttaagaggagtaaaagattttttgtagaataataactatattcagattatactttgttcttgaaaaaattacagattttttgaaaagcaaatgatgtaactcaactcattatttctgciguccuc gttaagaggagtaaaagattttttgtagaataataactatattcagattattcagattgtagagattattatagattgtagagattatttat

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Consensus includes gui. N. 133355 //UG=Hs. 133355 //UG=Hs. 133355 EST sacacticcagctigitigateacagatinnacaegatignactigaageteceteaatigaaaaee ctetteeteagetetteateatetaeagatigeagecageaeggticateatetigaggaateeaceaag ttatecaatatiggaaagggtatetetetetogaeggeagaaeaeagagagtgaeetaaaagaa tatecaatatigaaaagggtatetetetogaeggeagaaaaagaeageetigaaaaaaaaaaaaaaaaa	gb Al498747	235818 at
	gb A 492051	235753 at
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Consensus includes gp. bE32003/ / EXTENDED AND AND AND AND AND AND AND AND AND AN	gb BE326857	235719_at
accagcctggccaacatggtgaaaccccatntnnacta		

Consensus includes gp:AWZ9400077 EA-EST 700077 EA-EST 7000	gb AW294080	236226_at
Consensus includes gb. br 3 10-57.72 ESTs, Weakly similar to unknown /CLONE=IMAGE:3084166 /UG=Hs.115772 ESTs, Weakly similar to unknown /CLONE=IMAGE:3084166 /UG=Hs.1157772 ESTs, Weakly similar to unknown /CLONE=IMAGE:3084166 /UG=Hs.1167772 ESTs, Weakly s	gb BF516337	236190_at
	gb Al076335	236019 at
/UG=Hs. 180644 /UG=Hs	gb AA677057	235982 at
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Consensus includes gb:AA789123 /FEA=EST /DB_XREF=gi:2849243 /DB_XREF=est:aa66f03.s1 /CLONE=IMAGE:825917 /UG=Hs.46645	gb AA789123	236301 at
Consensus includes gb:BE6/6336 /FEA=ES1 /DB_XREF=91.10000070 /NDF-XREF-91.10000070 /NDF-XREF-91.10000070 /NDF-XREF-91.10000070 /NDF-XREF-91.10000070 /NDF-XREF-91.10000070 /NDF-XREF-91.10000070 /NDF-XREF-91.10000070 /NDF-XREF-91.10000070 /NDF-XREF-91.10000070 /NDF-XREF-91.1000070 /N	ablBE676335	236293 at
Consensus includes gb:Al225238 /FEA=EST /DB_XKEF=gl:3807951 /DB_XKEF=gr:3807951 /DB_XK	gb Al225238	236280_at
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Claims

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- 1. A method of determining whether a patient sample contains leukemia cells or other cells comprising the steps of
 - a) determining the the expression profile of a group of markers in a patient sample and
 - b) concluding from expression profile whether the patient sample contains leukemia cells or other cells

characterized in

that the group of markers consists of markers selected independently from the
markers listed in one or more of the tables 3 to 6, tables 15 to 20, tables 29, 30, 41,
or 42 and whereby the number of markers in the group is between one and the
total number of markers listed in the tables 3 to 6, tables 15 to 20, and tables 29,
30, 41, or 42.

20 2. The method according to claim 1

characterized in that

the number of markers in the group is between two and the total number of markers listed in the tables tables 3 to 6, tables 15 to 20, and tables 29, 30, 41, or 42.

- The method according to claim 1 or 2
 characterized in
 that the group of markers consists of all markers listed in one or more tables,
 whereby the tables are selected from the tables 3 to 6, tables 15 to 20, and tables
- 30 29, 30, 41, or 42.

- 4. A method of determining whether a patient sample contains leukemia cells or other cells and at the same time or subsequently determining the type and subtype of leukemia cells, if leukemia cells are present, comprising the steps of
 - a) determining the expression profile of a group of markers in a patient sample and
- b) concluding from the expression profile whether the patient sample contains leukemia cells or other cells and at the same time or subsequently determining the type and subtype of leukemia cells, if leukemia cells are present, characterized in
- that the group of markers consists of markers selected independently from the
 markers listed in one or more of the tables 16 to 20 or table 29 or 30 and whereby
 the number of markers in the group is between one and the total number of
 markers listed in the tables 16 to 20 or table 29 or 30.
 - 5. The method according to claim 4
- 15 characterized in that the number of markers in the group is between two and the total number of markers listed in the tables 16 to 20 or table 29 or 30.
 - 6. The method according to claim 4 or 5
- 20 characterized in that the group of markers consists of all markers listed in one or more tables, whereby the tables are selected from the tables 16 to 20 or table 29 or 30.
 - 7. The method according to any of claims 4 to 6
- characterized in that it is differentiated between four types of leukemia cells in the patient sample and that the other cells are normal cells.
- 8. The method according to any of claims 1 to 7
 30 characterized in that at least one marker is selected from the group consisting of
 ADCY3.
 - adenosine deaminase (ADA),

- ARGHGAP4,
- B-cell, a specific coactivator of octamer binding transcription factors,
- CAPN3, a member of the papain superfamily,
- CBFB-MYH11,
- 5 CD24,
 - CD27,
 - CD74,
 - connective tissue growth factor (CTGF),
 - CTGF,
- 10 CTSW,
 - MYH11
 - glucocorticoid receptor beta
 - CBFA2T1 (formerly ETO)
 - HLA-DMB
- 15 HOXA9
 - HOXB5
 - IRF4, an immune system-restricted interferon regulatory factor
 - KIAA1013
 - LCN2, a modulator of inflammation
- 20 LEF-1
 - MBNL
 - MSF translocation partner of the mixed-lineage leukemia gene (MLL) in AML
 - NCOA1,
 - OS-9
- 25 Phospholipidscramblase 1 (PLSCR1)
 - POU2AF1
 - POU2F2
 - POU4F1
 - SCYA3
- 30 DEFA3, SGP28, CAMP, CLC

SOCS-2 and

- TRB and CD3D
- 9. A method of differentiating between two types of leukemia cells or one type of
 5 leukemia cells and normal cells or non-leukemia in a patient sample comprising the
 steps of
 - a) determining the expression profile of a group of markers in the patient sample and
- b) concluding from the expression profile which type of leukemia cells the patient sample contains or whether it contains normal cells or non-leukemia characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 3 to 6 or tables 7 to 12 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 3 to 6 or tables 7 to 12.
- 10. The method according to claim 9
 characterized in that
 the number of markers in the group is between two and the total number of
 markers listed in one or more of the tables 3 to 6 or tables 7 to 12.
- 11. The method according to claim 9 or 10
 characterized in
 that the group of markers consists of all markers listed in one or more of the tables
 3 to 6 or tables 7 to 12.
 - 12. A method of differentiating between the subtypes of AML cells or the subtypes of AML cells and normal cells in a patient sample comprising the steps of a) determining the expression profile of a group of markers in the patient sample and
 - b) concluding from the expression profile which subtypes of AML cells the patient

sample contains or whether it contains normal cells characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36 and whereby the number of markers in the group is between one and the total number of markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36.

13. The method according to claim 12 characterized in that

- the number of markers in the group is between two and the total number of markers listed in the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36.
 - 14. The method according to claim 12 or 13 characterized in
- that the group of markers consists of all markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36.
 - 15. The method according to any of claims 12 to 14 characterized in
- 20 that three, four or more subtypes of AML cells are determined.
 - 16. A method of assessing the efficacy of a test compound for inhibiting leukemia, the method comprising comparing the expression profile of a group of markers in a first sample obtained from the patient and maintained in the presence of the test
- compound and the expression profile of a group of markers in a second sample obtained from the patient and maintained in the absence of the test compound, wherein a significantly altered expression profile of the group of markers in the first sample, relative to the second sample, is an indication that the test compound is efficacious for inhibiting leukemia in the patient
- 30 characterized in that the group of markers consists of markers selected independently from the

markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

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- 17. A method of assessing the efficacy of a therapy for inhibiting leukemia in a patient, the method comprising comparing the expression profile of a group of markers in a first sample obtained from the patient prior to providing at least a portion of the therapy to the patient and the expression profile of a group of markers in a second sample obtained from the patient following provision of the portion of the therapy, wherein a significantly altered expression profile of the marker(s) in the second sample, relative to the first sample, is an indication that the therapy is efficacious for inhibiting leukemia in the patient characterized in
- that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

- 18. A method of selecting a composition for inhibiting leukemia in a patient, the method comprising:
 - a) separately maintaining aliquots of cells of a patient sample in the presence of a plurality of test compositions;
- 25 c) comparing the expression profile of a group of markers in each of the aliquots, and
 - d) selecting one of the test compositions which induces an altered expression profile of the group of markers in the aliquot containing that test composition, relative to other test compositions
- 30 characterized in that the group of markers consists of markers selected independently from the

markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

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- 19.A method of determining new subtypes of leukemia cells, the method comprising:
 - a) determining the expression profile of a group of markers of leukemia cells of unknown subtype
- b) comparing the expression profile of said leukemia cells of ??? subtype to the
 expression profile of a group of markers of leukemia cells of known subtype(s),
 thereby concluding that a new subtype is determined when the expression profile is
 different to all known subtypes,

characterized in

- that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
- 20 20.A method for guiding the therapy of leukemia in a patient depending on the leukemia subtype and/or the risk of relapse of disease, the method comprising:a) determining the expression profile of a group of markers in the patient sample, and
 - b) deciding about the therapy strategy depending on the leukemia subtype and/or the risk of relapse of disease

characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25

2442

or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

- 21.A method for monitoring the progression of leukemia in a patient, the method comprising:
- a) determining the expression profile of a group of markers in a patient sample at a first point in time, and
 - b) repeating step a) at a subsequent point in time; and
 - c) comparing the expression profile detected in steps a) and b) , and therefrom monitoring the progression of leukemia in the patient,
- that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
 - 22. The method of claim 21, wherein between the first point in time and the subsequent point in time, the patient has undergone chemotherapy.
- 20 23. The method according to any of the claims 1 to 22, wherein a transcribed polynucleotide or portion thereof is the marker or at least one of the markers.
 - 24. The method of claim 23, wherein the transcribed polynucleotide is a mRNA.
- 25 25. The method of claim 23, wherein the transcribed polynucleotide is a cDNA.
 - 26. The method according to any of claims 23 to 25, wherein the step of determining the expression profile further comprises amplifying the transcribed polynucleotide.
- 30 27. The method according to any of the claims 23 to 26, wherein the expression profile of the group of transcribed polynucleotides is determined by annealing the

2443

transcribed polynucleotides with a complementary polynucleotide or a portion thereof under stringent hybridization conditions.

- 28. The method according to any of the claims 1 to 27, wherein the patient sample is blood or bone marrow.
 - 29. The method according to any of the claims 1 to 22, wherein a protein is the marker or at least one of the markers.
- 10 30. The method of claim 29, wherein the expression profile of the proteins is detected using a reagent which specifically binds to one of the proteins.
 - 31. The method of claim 30, wherein the reagent is selected from the group consisting of an antibody, an antibody derivative, and an antibody fragment.

32. The method according to any of claims 16 to 31
characterized in that
the number of markers in the group is between two and the total number of
markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36,
38, 39, 41, 42.

- 33. The method according to any of claims 16 to 32
 characterized in
 that the group of markers consists of all markers listed in one or more of the tables
 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
 - 34. A kit for assessing the suitability of each of a plurality of compounds for inhibiting leukemia in a patient, the kit comprising:
- a) (optionally) a plurality of compounds; and
 - b) a reagent for assessing the expression profile of a group of markers

characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

- 35. A kit for assessing whether a patient is afflicted with leukemia, the kit comprising reagents for assessing the expression profile of a group of markers
- that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
 - 36. A kit for assessing the presence of human leukemia cells, the kit comprising an antibody, wherein the antibody specifically binds with a protein corresponding to a marker
- 20 characterized in that the marker is selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
- 37. A kit for assessing the leukemia cell carcinogenic potential of a test compound, the kit comprising leukemia cells and a reagent for assessing expression of a marker, wherein the marker is selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
- 38. A protein or mRNA, cDNA or cRNA corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 for the treatment of leukemia.

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2445

39. A method for the preparation of a pharmaceutical composition for the treatment of leukemia

characterized in

- that a protein corresponding to a marker selected from the tables 1 to 20, tables 25 5 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds.
- 40. A method for the preparation of a pharmaceutical composition for the treatment of leukemia 10

characterized in

that a vector comprising a polynucleotide encoding a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds.

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41. A method for the preparation of a pharmaceutical composition for the treatment of leukemia

characterized in

that an antisense oligonucleotide complementary to a polynucleotide encoding a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 20 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds.

- 42. Use of a marker or a group of markers selected individually from one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 for 25 the determination of leukemia cells, the type or subtype of leukemia cells.
- 43. Use of a marker or a group of markers selected individually from one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 or 36for the determination of the subtype of AML cells. 30

44. A composition comprising a group of markers and substances chemically different to the markers

characterized in

that the group of markers consists of markers selected independently from the
markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30,
32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is
between one and the total number of markers listed in the tables 1 to 20, tables 25
or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

10 45. The composition according to claim 44

characterized in

that the group of markers consists of all markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

15 46. The composition according to claim 45

characterized in

that the group of markers consists of all markers listed in one or more of the tables 14 or tables 16 to 20 or table 29 or 30.

20 47. The composition according to claim 46

characterized in

that the group of markers consists of all markers listed in the tables 16 to 20 or table 29 or 30.

25 48. The composition according to claim 44 to 47

characterized in

that the markers are polynucleotides or oligonucleotides and are bound to a solid phase in the form of an array.

30 49. A method of determining the subtypes of ALL cells in a patient sample comprising the steps of

2447

- a) determining the level of expression of a group of markers in the patient sample and
- b) concluding from the differences in the level of expression which subtypes of ALL cells the patient sample contains
- 5 characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 18, 32 or 33 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 18, 32 or 33.

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50. The method according to claim 49

characterized in

that the group of markers consists of all markers listed in one or more of the tables 18, 32 or 33.

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- 51. A method of determining the subtypes of CLL cells in a patient sample comprising the steps of
 - a) determining the level of expression of a group of markers in the patient sample and
- 20 b) concluding from the differences in the level of expression which subtypes of CLL cells the patient sample contains

characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 38 or 39 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 38 or 39.

- 52. The method according to claim 51 characterized in
- 30 that the group of markers consists of all markers listed in one or more of the tables

38 or 39.

- 53. A method of determining whether a patient sample contains leukemia cells or other cells and at the same time determining the type and subtype of leukemia cells,
- 5 comprising
 - a) providing a patient sample,
 - b) isolating RNA from the patient sample, transcribing the RNA into cDNA and transcribing the cDNA into cRNA while simultaneously labelling the cRNA
 - c) hybridising the cRNA to a microarray having attached thereto a group of markers selected from the group listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38,. 39, 41, 42 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38,. 39, 41, 42, and d) determining the level of expression of a marker or a group of markers.

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- 54. Use of a marker or a group of markers selected from the group of members contained in the appended tables for determining whether a patient sample contains leukemia cells or other cells.
- 20 55. Use of claim 54 wherein said determination comprises the simultaneous determination of the type and subtype of leukemia cells.